

Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
43.00	100.00%	100.00%	5.93%	43	0	0	0	0
US-10-735-098-2 (1-725) x BD074758 (1-2262)								
QY	171	ArgLeuGLYTYrAspGIyPheValTYrTYrSergYGLuArgProSerGlnSerLeuPro	190					
Db	526	CGCTTAGGTTAAAGACGGTTTGTATATATATTCGGAGAACGTCCTTCATCTTACCG	585					
QY	191	SerAlaGLYThValGluTYrSergYAsnTPGInTYrMetThrAspAlaYSargHis	210					
Db	566	AGTCGGGAAACGGTGAATATTCGTGAATCTGCAATATATATGACCAATATGCCAAAGCAT	645					
QY	211	ArgAlaGLY 213						
Db	646	CGACGACGT 654						
RESIDUE 72								
LOCUS	AF072890	2519 bp	DNA	linear	BC1 22-JAN-1999			
DEFINITION	Neisseria gonorrhoeae lactoferrin binding protein B precursor							
ACCESSION	AF072890	(lbpB) gene, complete cds.						
VERSION	AF072890.1	GI:4106392						
KEYWORDS								
SOURCE	Neisseria gonorrhoeae							
ORGANISM	Neisseria gonorrhoeae; Bacteriobacteriales; Neisseriales; Neisseria							
REFERENCE	Biswas,G.D., Anderson,J.E., Shen,C.J., Corneliussen,C.N. and Sparling,P.F. Identification and functional characterization of the Neisseria gonorrhoeae lbpB gene product							
AUTHORS	Infect. Immun. 67 (1), 455-459 (1999).							
TITLE	Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521							
JOURNAL	Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA							
FEATURES	Location/Qualifiers							
source	1. 2519							
	/organism="Neisseria gonorrhoeae"							
	/mol_type="genomic DNA"							
	/strain="F49"							
	/db_xref="taxon:485"							
	184..209							
	/note="putative"							
	276..2496							
	/gene="lbpB"							
	276..293							
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	/note="putative"							
	/bound_moiety="FUR"							
	301..304							
	/gene="lbpB"							
	310..2496							
	/note="lbpB"							
	/codon_start=1							
	/transl_table=1							
	/product="lactoferrin binding protein B precursor"							
	/protein_id="AAD08809.1"							
	/db_xref="GI:4106393"							
	/transl_table=1							
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	DVFLEFGKGNKTLQOLKSEIHRSDVETRTSEKKKGYEIVDGYTTTKGDEI							
	EONSQGRKFTHRFGYDGFYVYSGERSQSILPSAGTVKTRFMWQYMTDARKHRTGKVA							

2

sig_peptide
mat_peptide
misc_feature
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-735-098-2 (1-725) x AF072890 (1-2519)
Qy 101 GIUCLVSPVAlleuPheLeuTYRgISerLYGclYAsnLYsleuGInGInLeuLYSer 120
Db 610 GAAGGTATGTTCTGTTTATACGGTCAAAAGAAATTAACCTTACAAACCTTAAAGC 669
Qy 121 GIUllleHisLYsARgAspSerAspValGluileArGThrSerGluLYsGluAsnLYsLYs 140
Db 670 GAATTATATAAGCTGATTCGATGTAGAAATTAGACGTCAGAAAGGAAATTAATAAAA 729
Qy 141 TYR 141
Db 730 TAT 732
RESULT 23
LOCUS NGU16260
DEFINITION Neisseria gonorrhoeae lactoferrin receptor precursor (lbpA) gene,
complete cds.
ACCESSION U16260.1 GI:915277
VERSION u16260
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .3300
/organism="Neisseria gonorrhoeae"
/mol_type="genomic DNA"
/strain="FA19"
/specific_host="Homo sapiens"

BT5WU5p9.1

BEST AVAILABLE COPY

protein_bind /db_xref="taxon:485"
162.180
/note="potential fur binding site"
/bound_molec="Fur"
RBS 268.272
/gene="lbpA"
278.3109
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278.3109
/note="Pre-lbp1"
/codon_start=1
/transl_table=11
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/protein_id="AAC13780.1"
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VAAKAGRSKEATGLKIVTSETLNKGQVIGIRLTYDGVAVVEGNAAGS
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SSDHGSGALGAAVAPRTKADLISDGKMGIOAKTAVGSKROPKWIKGAGPDKG
EGLLITTEQCRTPRHGDIADGVEGIRLDAFRTYDIKKTTPFPLVGEENTLK
PAKLAGYGIYLNRLQNRWKEIEONQPLSAEEOVEAOEHNLSAQAIVTGGR
1LPDMDYSGSWLALGYRFGGRHYGVGFEDTKORYDIRMTERKYTGDEAEKFR
DSGVYDGDPRDLGVFNIEBKGDKNLKGKGLKYSRTKFDHHRHRRMGLYR
YENEXYSDMAADKAVLSPDKGVATDNTLKLNCAYPAVDKSCRAADKPYSDSD
RHHYRQHVLNLSPEKSKKWTGHTLGRGVDAKVSREPOLSHAAIISSTG
FBEKNDKTRLGKPEVBSVCSYITTLASRCKVPRKINSNHIISLNRFSIGKFD
FSLGGRYDRKNTTSELVRSGRYADRSWNSGVIFKPNHFSVSVASGFPSTFOE
LEGLIDYHYDKMQRPAKSEKXANREGLQWKGDFLEISFENRYTDMIAVADQ
KTYLIPDSAGRLTEIDIRDYNAQMSLOGINIGKIDMNGVYKLEPGLYTLAVNR
KRSVSNRPDLISRLYALDAVOPSRVGLGQYOPGKMGANMLYVSKGNPDLAY
LACDOKRYAGRTSSMTADVASLYNLKRLTLRAIYNIGRYVTVESLRQNTES
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350.3106
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/product="lactoferrin receptor"
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829.838
/gene="lbpA"
/note="DNA uptake sequence"
3117.3126
/note="DNA uptake sequence"
ORIGIN
Alignment Scores:
Pred. No.: 2.3e-13 Length: 3300
Score: 22.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.03% Indels: 0
DB: 1 Gaps: 0
US-10-735-098-2 (1-725) x NGUI6260 (1-3300)
QY 704 ProGluValIysPProGlnPheGlyValIValPheGlyAlaIysAspAsnLysGluVal 723
Db 213 CCTGAAGTTAAACCCCAATTCGGCTGATTCGGTCGAAAGAAAGTATATAAGAGGTG 272
QY 724 GluLys 725
Db 273 GAAAAA 278
RESULT 24
LOCUS AX685922 3300 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 80 from Patent WO02062380.
ACCESSION AX685922
VERSION AX685922.1 GI:29371832
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1

815278
lbpA
b

AUTHORS Berthel, F.X., Lobet, Y., Poolman, J., and Verlaan, V.
TITLE Chlamydia vaccine composition
JOURNAL Patent: WO 02062380-A 80 15-AUG-2002;
GlaxoSmithKline Biologicals (BE)
FEATURES
source
1.3300
/organism="Neisseria gonorrhoeae"
/mol_type="unassigned DNA"
/db_xref="taxon:485"
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Alignment Scores:
Pred. No.: 1.26e-11 Length: 1000
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.76% Indels: 0
DB: 6 Gaps: 0
US-10-735-098-2 (1-725) x AX081510 (1-1000)
QY 427 AlaCysCysAspPheLeuThrTyValIysLeuGlyArgIleIysThrGluArgProAla 446
Db 106 GCTTGTGGACCTTTTGAACCTATGGAACCTCGACGATTAACCAACGCGCCGCA 165
RESULT 26
LOCUS AX374691 1000 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 15 from Patent WO0209746.
ACCESSION AX374691
VERSION AX374691.1 GI:19169587
US-10-735-098-2 (1-725) x AX081510 (1-1000)
QY 704 ProGluValIysPProGlnPheGlyValIValPheGlyAlaIysAspAsnLysGluVal 723
Db 213 CCTGAAGTTAAACCCCAATTCGGCTGATTCGGTCGAAAGAAAGTATATAAGAGGTG 272
QY 724 GluLys 725
Db 273 GAAAAA 278
RESULT 25
LOCUS AX081510 1000 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 15 from Patent WO0109350.
ACCESSION AX081510
VERSION AX081510.1 GI:13170329
KEYWORDS
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1
AUTHORS Berthel, F.X., Dalemans, W.L., Denoel, P., Deguesne, G.S., Feron, C.S.,
Lobet, Y.S., Poolman, J.S., Thiry, G.S., Lhonnard, J.S. and Voet, P.S.
TITLE Genetically engineered bleb vaccine
JOURNAL Patent: WO 0109350-A 15 08-FEB-2001;
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
FEATURES
source
1.1000
/organism="Neisseria meningitidis"
/mol_type="unassigned DNA"
/db_xref="taxon:487"
ORIGIN
Alignment Scores:
Pred. No.: 1.26e-11 Length: 1000
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.76% Indels: 0
DB: 6 Gaps: 0
US-10-735-098-2 (1-725) x AX081510 (1-1000)
QY 427 AlaCysCysAspPheLeuThrTyValIysLeuGlyArgIleIysThrGluArgProAla 446
Db 106 GCTTGTGGACCTTTTGAACCTATGGAACCTCGACGATTAACCAACGCGCCGCA 165
RESULT 26
LOCUS AX374691 1000 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 15 from Patent WO0209746.
ACCESSION AX374691
VERSION AX374691.1 GI:19169587

US-10-735-098-2 (1-725) x AAT11243 (1-2070)
 QY 649 G1yG1yPheTyRG1yProTySaLaG1uG1uLeuG1yG1y 661
 DB 1912 GCGGGTTTACGGGCTTAAGCCGAAGAGTTGGCGGA 1950

RESULT 21

AAT11241
 ID AAT11241 standard; DNA; 2114 BP.

AC AAT11241;

XX 16-OCT-2003 (revised)

DT 02-SEP-1996 (first entry)

XX Neisseria meningitidis strain 6940 transferrin receptor Tbp2 gene.

XX Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;

XX passive immunisation; immunotherapy; IM2169; ss.

XX Neisseria meningitidis; (strain 6940).

OS Key Location/Qualifiers

FT CDS 1..2082

FT mat_peptide 1..2079

FT /*tag= a

FT /*tag= b

XX WO9533049-A2.

XX 07-DEC-1995.

XX 30-MAY-1995; 95MO-FR000701.

XX 31-MAY-1994; 94FR-00006594.

XX (INMR) PASTEUR MERIEUX SERUMS & VACCINS.

XX (TRGE) TRANSGENE SA.

XX M11let MBJ, Lissolo L, Mazarin V, Legrain M, Jacobs E;

XX MPI; 1996-030562/03.

XX P-PSDB; AAR88646.

XX Polypeptide(s) for vaccination against Neisseria meningitidis group B -

XX comprising deletion mutants of transferrin receptor Tbp2 subunit.

XX Disclosure; Page 53-56; 114p; French.

XX The present sequence is that of the N.meningitidis strain 6940

XX transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an

XX N-terminal domain, a hinge domain and a C-terminal domain; deletion

XX mutants in which at least one of the domains is partially or totally

XX deleted are claimed, provided that the first and second domains are not

XX simultaneously partially or totally deleted. Strain 6940 is an IM2169-

XX related N.meningitidis strain and the positions of the 3 domains are

XX defined by alignment with the IM2169 sequence. The deletion mutant

XX polypeptides of the invention can generate an immune response against

XX N.meningitidis. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 2114 BP; 695 A; 478 C; 511 G; 430 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177 Length: 2114

Score: 13.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.79% Indels: 0

DB: 2 Gaps: 0

US-10-735-098-2 (1-725) x AAT11241 (1-2114)

QY 649 G1yG1yPheTyRG1yProTySaLaG1uG1uLeuG1yG1y 661

DB 1936 GCGGGTTTACGGGCTTAAGCCGAAGAGTTGGCGGA 1974

RESULT 22

AAT11242
 ID AAT11242 standard; DNA; 2114 BP.

AC AAT11242;

XX 16-OCT-2003 (revised)

DT 02-SEP-1996 (first entry)

XX Neisseria meningitidis strain S3032 transferrin receptor Tbp2 gene.

XX Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;

XX passive immunisation; immunotherapy; IM2169; ss.

XX Neisseria meningitidis; (strain S3032).

OS Key Location/Qualifiers

FT CDS 1..2100

FT mat_peptide 1..2097

FT /*tag= a

FT /*tag= b

XX WO9533049-A2.

XX 07-DEC-1995.

XX 30-MAY-1995; 95MO-FR000701.

XX 31-MAY-1994; 94FR-00006594.

XX (INMR) PASTEUR MERIEUX SERUMS & VACCINS.

XX (TRGE) TRANSGENE SA.

XX M11let MBJ, Lissolo L, Mazarin V, Legrain M, Jacobs E;

XX MPI; 1996-030562/03.

XX P-PSDB; AAR88647.

XX Polypeptide(s) for vaccination against Neisseria meningitidis group B -

XX comprising deletion mutants of transferrin receptor Tbp2 subunit.

XX Disclosure; Page 58-61; 114p; French.

XX The present sequence is that of the N.meningitidis strain S3032

XX transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an

XX N-terminal domain, a hinge domain and a C-terminal domain; deletion

XX mutants in which at least one of the domains is partially or totally

XX deleted are claimed, provided that the first and second domains are not

XX simultaneously partially or totally deleted. Strain S3032 is an IM2169-

XX related N.meningitidis strain and the positions of the 3 domains are

XX defined by alignment with the IM2169 sequence. The deletion mutant

XX polypeptides of the invention can generate an immune response against

XX N.meningitidis. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 2114 BP; 691 A; 493 C; 509 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177 Length: 2114

Score: 13.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.79% Indels: 0

DB: 2 Gaps: 0

US-10-735-098-2 (1-725) x AAT11242 (1-2114)

QY 649 G1yG1yPheTyRG1yProTySaLaG1uG1uLeuG1yG1y 661

DB 1942 GCGGGTTTACGGGCTTAAGCCGAAGAGTTGGCGGA 1980

Iron uptake protein; transferrin binding protein, TbpA, TbpB, vaccine;
neisserial disease; meningococcal disease; gonococcal disease;
antimicrobial; antibacterial; ds.

Neisseria meningitidis.

Location/Qualifiers
Key 1.2139
/tag= a
/product= "Neisseria meningitidis TbpB protein"

W0200173080-A2.

04-OCT-2001.

27-MAR-2001; 2001WO-GB001348.

27-MAR-2000; 2000GB-00007433.

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

Gorringe AR, Hudson MJ, Matheson MA, Robinson A, West DM,

WPI; 2001-616522/71.

P-PSDB; AAE12019.

Non-neisserial cells useful in manufacturing of vaccines without the loss of antigenicity of the native protein, against meningococcal diseases such as meningitis, express a recombinant neisserial iron uptake protein.

Example 1; Page 19-21; 57pp; English.

The present invention relates to a non-neisserial cell expressing a neisserial iron uptake protein, where neisserial iron uptake proteins including transferrin binding protein (Tbp) A and TbpB can be extracted from the cell under mild conditions and retains substantially the antigenicity of native iron uptake protein. The non-neisserial cell is useful in manufacture of Tbp, and in the manufacture of vaccines for protection against neisserial disease, meningococcal disease and/or gonococcal disease. The affinity matrix is useful for purifying a Tbp, where Tbp containing preparation is eluted through the matrix. The present sequence is a Neisseria meningitidis strain K454 (TbpB gene

Sequence 2139 BP; 696 A; 492 C; 519 G; 432 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	0.0179	Length:	2139
Percent Similarity:	13.00	Matches:	13
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	1.79%	Mismatches:	0
		Indels:	0
		Gaps:	0

-10-735-098-2 (1-725) x AAD19530 (1-2139)

649 GYGYPhetyrGlyProlysaGluGluLeuGlyGly 661
1993 GCGGTTTTTACGGGCCCAAGCCGAAGAGTTGGCGCA 2031

JUL 26

AA055619 standard; DNA; 2230 BP.

AA055619;

16-OCT-2003 (revised)

25-MAR-2003 (revised)

15-JUL-1994 (first entry)

N.meningitidis IM2169 transferrin receptor Tbp2 subunit DNA sequence.

Transferrin receptor; Tbp2 subunit; strain IM2169; meningitis vaccine;

KW Iron transport protein; iron chelator; ss.
XX
OS Neisseria meningitidis; (strain IM2169).

Key Location/Qualifiers

FT CDS 60..2195
FT /tag= a
FT sig_peptide 60..119
FT /tag= b
FT mat_peptide 120..2192
FT /tag= c
FT /product= "Tbp2"

FR692592-A1.

24-DEC-1993.

19-JUN-1992; 92FR-00007493.

19-JUN-1992; 92FR-00007493.

(INMR) PASTEUR MERIEUX SERUMS & VACCINS.

(TRGE) TRANSGENE SA.

Jacobs E, Legrain M, Mazarin V, Bouchon-Theisen B, Shryvers AB;

WPI; 1994-028254/04.

P-PSDB; AAR48222.

DNA coding for neisseria meningitidis proteins - namely transferrin receptor subunits.

Claim 2-7 and 11-12; Page 36-40; 60pp; French.

Sequences coding for the Tbp1 and Tbp2 transferrin receptor subunits were isolated from a Neisseria meningitidis strain IM2169 genomic DNA library (see AA055618 and AA055619, respectively). Cells transformed with the DNA can be used for large scale production of the receptor proteins. (Updated on 25-MAR-2003 to correct PV field.) (Updated on 16-OCT-2003 to standardise OS field)

Sequence 2230 BP; 727 A; 483 C; 547 G; 473 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	0.0186	Length:	2230
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.79%	Indels:	0
DB:		Gaps:	0

US-10-735-098-2 (1-725) x AA055619 (1-2230)

649 GYGYPhetyrGlyProlysaGluGluLeuGlyGly 661
2037 GCGGTTTTTACGGGCCCTAAAGCCGAAGAGTTGGCGCA 2075

RESULT 27

AA11238 standard; DNA; 2230 BP.

AA11238;

16-OCT-2003 (revised)

30-AUG-1996 (first entry)

Neisseria meningitidis strain IM2169 transferrin receptor Tbp2 gene.

Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;

passive immunisation; immunotherapy; ss.

Neisseria meningitidis; (strain IM2169).

~~MAIL WITH~~ Office Action

DQKRYSTKRASSWSWSTADVAYLNLKKRLTLRAIYINIGNRYVTWESLRQTAESTAN
RHGGSNRYGRYAAPGRNFSLAEMKF"

Gaps:

3981

[illegible]

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 Db 1379 CAGCAAGCAACAGCGCTATTCGGGTATTCGCGAGCAACCAATATACCCCGTCCGCTC 1438
 Qy 360 rGlyLysHisThrValLeuAspSerLeuLysIleSerValAspGluAlaLysGlyVal 380
 Db 1439 TGGAAACACACCAAAATCTTGATTCCTGAAATTTCCGTTATAGGCAAGTGTGTA 1498
 Qy 380 uAsnProArgProPheAlaIleSerProMetProAspPheGlyValAspAspLysLeu 400
 Db 1499 AAATCCCGGACCGTTTCCATTTCTCTATGCGCGATTTGTCATCCGCAAACTTCT 1558
 Qy 400 uValGluGlyHisGlyIleProLeuValSerGluLysThrIleGluLeuAlaAspGly 420
 Db 1559 TGTTCGAAGGCGATGAATTCCTTGTGTTACCAAGAAACCATGAGCTTCCGACCG 1618
 Qy 420 YArgLysMetThrValSerAlaCysCysAspPheLeuThrValLysLeuGlyArgIle 440
 Db 1619 CAGGAAATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1678
 Qy 440 eLysThrGluArgProAlaAlaLysProLysAlaGluAspGluLysAspSerAspIleAs 460
 Db 1679 AAAAACCAGACCTCCGCGCGCAAAACCGAGCGAGCAAGAGATTGCGACATTGTA 1738
 Qy 460 PAsnGlyLysGluSerGluAspGluIleGlyAspGluGluGlyLysThrGluAspAla 480
 Db 1739 TAAATGCGCAAGAAACGAAAGCAAAATCGCGCATGAAGAGACCGCAAGATGCGAGC 1798
 Qy 480 AAlaGlyAspGluGlySerGluGluAspGluAlaThrGluAsnGluAspGlyValGlu 500
 Db 1799 CGCAGAGATGAAGCGAGCGAAAGCAAGACCGCAAGAAACGAGCGCGAGAAAGA 1858
 Qy 500 PGIuAlaGluGluProGluGluGluSerSerAlaGluGlyAsnGlySerSerAlaAla 520
 Db 1859 CGAAGCTGAAGAACTTAAGAGAAATCGTGGCGAGAAAGCGAGCTTCAAAACGCGCAT 1918
 Qy 520 eLeuProValProGluAlaSerLysGlyArgAspIleAspLeuPheLeuLysGlyIle 540
 Db 1919 CCGGCTGCTCCCGAAGCTCTAAAGCAGAGATATGAACTTTCTCTGAAAGATATCCG 1978
 Qy 540 gThrAlaGluThrAsnIleProGluThrGlyAlaLysGlyThrGlyThrTrpGluAl 560
 Db 1979 CACCGGAGAAAGCAATATTCGCGCAAACTGAGAGAGACGCTATACCGGCACTTGGAGAG 2038
 Qy 560 AArgIleGlyLysProIleGluThrAspAsnHisAlaAspLysGluAlaLysAlaVal 580
 Db 2039 GCGATCGGCAAAACCATTCATTCGAGCAATATGCGGATTAAGAAAGCGGCAAAAGCACT 2098
 Qy 580 lPheThrValAspPheGlyLysLysSerLysSerGlyThrLeuThrGluLysAsnGlyVal 600
 Db 2099 ATTTACCGTTGATTCGCGCAAGAAATTCATTTCCGGAACGCTGACGAGAGAAACCGGTGT 2158
 Qy 600 lGluProAlaPheArgIleGluAsnGlyValIleGluGlyAsnGlyPheHisAlaThrAl 620
 Db 2159 AGAACCTGCTTCCGATTTGAAACCGCGGTATTCAGGCAACGCTTCCATGCGACAGCC 2218
 Qy 620 AArgThrArgAspAspGlyIleAspLeuSerGlyLysLysSerThrLysProGluIlePhe 640
 Db 2219 GCGCACTCGGAGATACGCACTGACCTTTCCGCGCAGGCTTCGACAAACCGCAGATCTT 2278
 Qy 640 eLysValAspAspLeuArgValGluGlyLysPheTyrGlyProLysAlaGluGluLeuGly 660
 Db 2279 CAAGCTAAAGATCTTCTGTAGAGAGAGATTTTACGCGCCGAGAGCGGAGGATTTGGG 2338
 Qy 660 YGlyIleIlePheAspAsnAspGlyLysSerLeuGlyIleThrGluGlyLysThrGluAsn 680
 Db 2339 CGGTATTTATTTCAATATATATGAGAAATCTTGTGATACGAGAGTACTGAAATTA 2398
 Qy 680 sValGluAlaAspValAspValAspValAspValAspValAspValAspValAspVal 700
 Db 2399 AGTTGAAGCTGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2457

ORIGIN

mat_peptide

sig_peptide

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

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720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

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720 snLysGluValGluLys 725

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

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720 snLysGluValGluLys 725

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720 snLysGluValGluLys 725

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

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720 snLysGluValGluLys 725

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

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2518 ATTAAGAGGTGAGAAAA 2534

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

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2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

2518 ATTAAGAGGTGAGAAAA 2534

720 snLysGluValGluLys 725

2458 AACAGTTAAACCTGAGATTAAACCCCATTCGCGCGTGTGATTCGGTGGAGAAAGATA 2517

700 lGluLysLeuLysProGluValIleLysProGluPheGlyValAlaLysLysAsp 720

Alignment Scores:

Pred. No.: 3, 766-67
 Score: 70.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 9.66%
 DB: 1
 Length: 3171
 Matches: 70
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-735-098-2 (1-725) x NMIR0A (1-3171)

OY 656 Aaagiugluuuglygyllellephehenaanaapgllyserleuglylerhgu 675
 Db 20 GCGGAGGATTCGGCGGATTTATTTCAATATGATGGAATCTCTGATTAAGTGA 79
 OY 676 GYTHRGUaenlyvaigluuaspvalaspvalaspvalaspvalaspala 695
 Db 80 GGTACTGAAAATAAGTTGAGACCTATGATGTTGATGTTGATGATGATCT 139
 OY 696 Aspaiaapvalaigluuenuyprogluvalylsproglnphaglyvalaaphagly 715
 Db 140 GATGCTGATTTGAACAGTTAAACCTGAAGTTAAACCCCAATTCGGGCTGATTCGT 199
 OY 716 Aaalylyaspaanlysglyuvalglubys 725
 Db 200 GCGAGAAAAGATTAATAAGAGGTGAAAAA 229

RESULT 7

AF123380 2226 bp DNA linear BCT 24-MAY-1999
 LOCUS Neisseria meningitidis strain H44/76 lactoferrin-binding protein
 DEFINITION precursor (lbpB) gene, complete cds.
 ACCESSION AF123380
 VERSION AF123380.1 GI:4884686
 KEYWORDS Neisseria meningitidis
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
 Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 1 (bases 1 to 2226)
 Petersson, A., van der Biesen, J., Joosten, V., Hendriksen, J. and
 Tommaseen, J.
 Sequence variability of the meningococcal lactoferrin-binding
 protein lbpB
 JOURNAL Gene 231 (1-2), 105-110 (1999)
 MEDLINE 99250255
 PUBMED 10231574
 REFERENCES 2 (bases 1 to 2226)
 Petersson, A., van der Biesen, J., Joosten, V., Hendriksen, J. and
 Tommaseen, J.
 TITLE Direct Submission
 JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology,
 Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
 FEATURES
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 /organism="Neisseria meningitidis"
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 EIWTSNRKQFSNRFYVYSGEHPQSILPSAGTVQSGNMQYMTDAIRHRTGA
 ADIPQTKARVGTGWEARISKPIQWNAHAKKAAKAFPDVDFEKSISGLTTEKNGVO
 PAFHENGVIENGFHATARTRDGILNSGNDSTNPSFRANNILVYGGYFQPAEEL
 GGTIFPNDGSLGTTEDTENEALEVENAGVGEQLKPEAKPQGVVFGAKKDKEVE
 K"

ORIGIN

Alignment Scores:
 Pred. No.: 9, 756-53
 Score: 57.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 7.86%
 DB: 1
 Length: 2226
 Matches: 57
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-735-098-2 (1-725) x AF123380 (1-2226)

OY 1 MetCyslyspProaenlygyllyllevalleuenuleuenuleuaseCyale 20
 Db 1 ATGTGTAACCGAATATGCGGCGATTCCTGTTGCCCTTACTTTGGCATCTTGATT 60
 OY 21 GYGLYasnphegllyuaglnprovaivaigluuserthyrprothralatyrprovalthr 40
 Db 61 GCGGCAATTCGCGGAGCCGCTGTGTGAATCAACGCGGCGGTGATCCCGTCACT 120
 OY 41 PhelyserlyaspaalProthProProProAlalyProserileglin 57
 Db 121 TTCAAGCTTGAAGAGCTTCCACCTCCGCCCTCCCAACTTCTATAGAA 171

RESULT 8

A98972 2226 bp DNA linear PAT 26-JAN-2000
 LOCUS Sequence 5 from Patent WO9909176.
 DEFINITION A98972
 ACCESSION A98972.1 GI:6781932
 VERSION A98972.1 GI:6781932
 KEYWORDS Neisseria meningitidis
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
 Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
 1 (bases 1 to 2226)
 Petersson, A.M. and Tommaseen, J.P.
 TITLE NEISSERIA LACTOFERRIN BINDING PROTEIN
 JOURNAL Patent: WO 9909176-A 5 25-FEB-1999;
 UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNKA MAR (NL)
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 EIWTSNRKQFSNRFYVYSGEHPQSILPSAGTVQSGNMQYMTDAIRHRTGA
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 DKGEELAGRIISNDNSVFGVAGKTNNAATNTNAMPSEKKTILINDLSIKISVDAT
 DKARPAISPLDPFGHDKLIVGEKIPVSEKTELADGKMTYRACDPLTYVK
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 EAENNGEEDDEEPEEPESPAEGGGSGGILPAPAPAGRIDILFLKGIKRAE
 ADIPQTKARVGTGWEARISKPIQWNAHAKKAAKAFPDVDFEKSISGLTTEKNGVO
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Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.93% Indels: 0
Gaps: 0

US-10-735-098-2 (1-725) x BD074758 (1-2262)

QY 171 ArgLeuGlyTyrAspGlyPheValTyrTyrSerGlyIuArgProSerGlnSerLeuPro 190
Db 526 CGCTTAGGTATGACGGCTTTGTATATTATCCGAGAACGCTCTTCCCATCTTTACCG 585

QY 191 SerAlaGlyThrAlaGlyTyrSerGlyAsnTyrGlnTyrMetThrAspAlaLysArgHis 210
Db 586 AGCGGGAACGGGTGAAATTCGTGACTGCGCAATATATGACCGCAACGTCAT 645

QY 211 ArgAlaGly 213
Db 646 CGAGCAGGT 654

RESULT 22
AF072890 2519 bp DNA linear BCT 22-JUN-1999
LOCUS Neisseria gonorrhoeae lactoferrin binding protein B precursor
ACCESSION AF072890 complete cds.
VERSION AF072890.1 GI:4106392
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 2519)
Biswas, G.D., Anderson, J.E., Eben, C.J., Cornelissen, C.N. and Sparling, P.F.
Identification and functional characterization of the Neisseria
gonorrhoeae lbpB gene product
Infect. Immun. 67 (1), 455-459 (1999)

JOURNAL
MEDLINE 99081783
PUBMED 9864256
REFERENCE 2 (bases 1 to 2519)
AUTHORS Biswas, G.D., Anderson, J.E., Cornelissen, C.N. and Sparling, P.F.
TITLE Direct Submision
JOURNAL Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521
Burnett Womack/CB 7030, Chapel Hill, N.C. 27599, USA
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/mol_type="genomic DNA"
/strain="FA19"
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310..2496
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sig_peptide
mat_peptide
misc_feature

ORIGIN

Alignment Scores:
Pred. No.: 9/22=35 Length: 2519
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.66% Indels: 0
Gaps: 0

US-10-735-098-2 (1-725) x AF072890 (1-2519)

QY 101 GAlGAlAspValLeuPheLeuTyrGlySerLysGlyAsnLysLeuGlnLeuLysSer 120
Db 610 GAAGGTGATGTTCTGTTTATACGTTCAAGAAATTAACCTTCAACACTTAAAGC 669

QY 127 GluIleHisLysArgAspSerAspValGluIleArgThrSerGlyLysGlnAsnLysLys 140
Db 670 GAAATTCATTAACGCGATTCCGATGTAGAAATTAGACGTCGAAAGAAATTAATAAA 729

QY 141 Tyr 141
Db 720 TAT 732

RESULT 23
NGU16260
LOCUS NGU16260 3300 bp DNA linear BCT 27-FEB-1996
DEFINITION Neisseria gonorrhoeae lactoferrin receptor precursor (lbpA) gene,
complete cds.
ACCESSION U16260
VERSION U16260.1 GI:916277
KEYWORDS
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 3300)
Biswas, G.D. and Sparling, P.F.
Characterization of lbpA, the structural gene for a lactoferrin
receptor in Neisseria gonorrhoeae
Infect. Immun. 63 (8), 2958-2967 (1995)

JOURNAL
MEDLINE 95347808
PUBMED 7622218
REFERENCE 2 (bases 1 to 3300)
AUTHORS Biswas, G.D.
TITLE Direct Submision
JOURNAL Submitted (24-OCT-1994) Gour D. Biswas, Dept. of Medicine/Div. of
Infect. Dis., University of North Carolina, 521 Burnett-Womack
CB#7030, Chapel Hill, NC 27599-7030, USA
FEATURES
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/organism="Neisseria gonorrhoeae"
/mol_type="genomic DNA"
/strain="FA19"
/specific_host="Homo sapiens"

ment Scores:

No.	0.0171	Length:	2040
e:	13.00	Matches:	13
ent Similarity:	100.00%	Conservative:	0
Local Similarity:	100.00%	Mismatches:	0
y Match:	1.79%	Indels:	0
		Gaps:	0

-0-735-098-2 (1-725) x AAX26576 (1-2040)

649 G1G1G1PheTYG1G1ProLYSA1aG1G1LeuG1G1Y 661
 1882 GCGGTTTACGGGCTTAAGCCGAAGATTGGCGGCG 1920

14-JUN-1999 (first entry)
 AAX26577 standard; DNA; 2058 BP.

14-JUN-1999 (first entry)

Tbpb coding sequence from Neisseria meningitidis strain 8680.
 Low molecular weight subunit; Tbpb; human transferrin receptor; htr;
 Neisseria meningitidis; vaccine; meningococcal infection; meningitis; ss.
 Neisseria meningitidis.

Key Location/Qualifiers
 CDS 1..2058
 sig_peptide 1..48
 mat_peptide 49..2058
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MO9907741-A1.
 18-FEB-1999.
 03-AUG-1998: 98WO-FR001730.
 07-AUG-1997: 97FR-00010301.

(INMR) PASTEUR MERIEUX SERUMS & VACCINS SA.
 Quentin-Millet M, Rokhi B;

WPI; 1999-190036/16.
 P-PSDB; AAY01525.

Vaccine containing small subunit of human transferrin receptor from
 Neisseria meningitidis - for treatment and prevention of meningitis.
 Disclosure; Page 40-43; 73pg; French.

The present sequence encodes the low molecular weight subunit (Tbpb) of
 the human transferrin receptor (htr) from a specific strain of Neisseria
 meningitidis that contains Tbpb-encoding DNA. Compositions containing
 Tbpb are used as vaccines for treatment or prevention of meningococcal
 infections, particularly meningitis

Sequence 2058 BP; 621 A; 477 C; 551 G; 409 T; 0 U; 0 Other;

Alignment Scores:

ed. No.:	0.0172	Length:	2058
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.79%	Indels:	0
		Gaps:	0

US-10-735-098-2 (1-725) x AAX26577 (1-2058)

Oy 649 G1G1G1PheTYG1G1ProLYSA1aG1G1LeuG1G1Y 661
 Db 1900 GCGGTTTACGGGCTTAAGCCGAAGATTGGCGGCGA 1938

RESULT 20
 AAT11243
 ID AAT11243 standard; DNA; 2070 BP.

AC AAT11243;
 DT 16-OCT-2003 (revised)
 DT 02-SEP-1996 (first entry)

Neisseria meningitidis strain B283 transferrin receptor Tbpb2 gene.
 Transferrin receptor; Tbpb2 subunit; deletion mutant; vaccine;
 passive immunisation; immunotherapy; IM2169; IM2394; ss.
 Neisseria meningitidis; (strain B283).

Key Location/Qualifiers
 CDS 1..2070
 sig_peptide 1..60
 mat_peptide 61..2067
 /*tag= c

MO9531040-A2.
 07-DEC-1995.
 30-MAY-1995: 95WO-FR000701.
 31-MAY-1994: 94FR-00006594.

(INMR) PASTEUR MERIEUX SERUMS & VACCINS.
 (TRGE) TRANSGENE SA.

Millet MBJ, Bissolet L, Mazarin V, Legrain M, Jacobs E;
 WPI; 1996-030562/03.
 P-PSDB; AAR8648.

Polypeptide(s) for vaccination against Neisseria meningitidis group B -
 comprising deletion mutants of transferrin receptor Tbpb2 subunit.

Disclosure; Page 76-81; 114pp; French.

The present sequence is that of the N.meningitidis strain B283
 transferrin Tbpb2 subunit gene. The Tbpb2 polypeptide has three domains: an
 N-terminal domain, a hinge domain and a C-terminal domain; deletion
 mutants in which at least one of the domains is partially or totally
 deleted are claimed, provided that the first and second domains are not
 simultaneously partially or totally deleted. The positions of the 3
 CC domains in B283 are defined by alignment with the IM2169 sequence. The
 CC deletion mutant polypeptides of the invention can generate an immune
 response against N.meningitidis. (Updated on 16-OCT-2003 to standardise
 OS field)

Sequence 2070 BP; 617 A; 472 C; 560 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.0173	Length:	2070
Score:	13.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.79%	Indels:	0
		Gaps:	0

Millet MBJ

US-10-735-098-2 (1-725) x AAT11243 (1-2070)

QY 649 G1yG1yPhetYrG1yProLySA1aG1uLcUeUg1yG1y 661
 1912 GGGCGTTTTCAGCGCCCAAGCCGAAAGAGTTGGCGGA 1950

RESULT 21

AAT11241 standard; DNA; 2114 BP.

AAT11241;

16-OCT-2003 (revised)
 02-SEP-1996 (first entry)

Neisseria meningitidis strain 6940 transferrin receptor Tbp2 gene.

Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
 passive immunisation; immunotherapy; IM2169; ss.

Neisseria meningitidis; (strain 6940).

Key Location/Qualifiers

CDS 1..2082

FT 1..2082

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

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FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

FT 1..2079

Handwritten: Miller & ...
 1912

Db 1936 GGGCGTTTTCAGCGCCCAAGCCGAAAGAGTTGGCGGA 1974

RESULT 22

AAT11242 standard; DNA; 2114 BP.

AAT11242;

16-OCT-2003 (revised)

02-SEP-1996 (first entry)

Neisseria meningitidis strain S3032 transferrin receptor Tbp2 gene.

Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
 passive immunisation; immunotherapy; IM2169; ss.

Neisseria meningitidis; (strain S3032).

Key Location/Qualifiers

CDS 1..2100

FT 1..2100

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

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FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

FT 1..2097

Sequence 2114 BP; 691 A; 493 C; 509 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177

Score: 13.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.79%

DB: 2

Gaps: 0

US-10-735-098-2 (1-725) x AAT11242 (1-2114)

QY 649 G1yG1yPhetYrG1yProLySA1aG1uLcUeUg1yG1y 661

Sequence 2114 BP; 691 A; 493 C; 509 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177

Score: 13.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.79%

DB: 2

Gaps: 0

US-10-735-098-2 (1-725) x AAT11242 (1-2114)

QY 649 G1yG1yPhetYrG1yProLySA1aG1uLcUeUg1yG1y 661

Sequence 2114 BP; 691 A; 493 C; 509 G; 421 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.0177

Score: 13.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.79%

DB: 2

Gaps: 0

US-10-735-098-2 (1-725) x AAT11242 (1-2114)

QY 649 G1yG1yPhetYrG1yProLySA1aG1uLcUeUg1yG1y 661

Iron uptake protein; transferrin binding protein; TbpA; TbpB; vaccine;
 neisserial disease; meningococcal disease; gonococcal disease;
 antiinflammatory; antibacterial; ds.
 Neisseria meningitidis.

Key Location/Qualifiers
 CDS 1..2139
 /tag= a
 /product= "Neisseria meningitidis TbpB protein"

MO20UT173080-A2.

04-OCT-2001.

27-MAR-2001; 2001MO-GB001348.

27-MAR-2000; 2000GB-00007433.

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

Gorringe AR, Hudson MJ, Matheson MA, Robinson A, West DM;

WPI; 2001-616522/71.

P-PSDB; AAE12019.

Non-neisserial cells useful in manufacturing of vaccines without the loss of antigenicity of the native protein, against meningococcal diseases such as meningitis, express a recombinant neisserial iron uptake protein.

Example 1; Page 19-21; 57pp; English.

The present invention relates to a non-neisserial cell expressing a neisserial iron uptake protein, where neisserial iron uptake proteins including transferrin binding protein (Tbp) A and TbpB can be extracted from the cell under mild conditions and retains substantially the antigenicity of native iron uptake protein. The non-neisserial cell is useful in manufacture of Tbp, and in the manufacture of vaccines for protection against neisserial disease, meningococcal disease and/or gonococcal disease. The affinity matrix is useful for purifying a Tbp, where Tbp containing preparation is eluted through the matrix. The present sequence is a Neisseria meningitidis strain K454 cpbB gene

Sequence 2139 BP; 696 A; 492 C; 519 G; 432 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	Score:	Length:	Matches:
1	0.0179	2139	13
2	13.00	100.00%	0
3	100.00%	100.00%	0
4	1.79%	Indels:	0
5	5	Gaps:	0

-10-735-098-2 (1-725) x AAD19530 (1-2139)

649 GlyGlyPheTyrGlyProLysAlaGluGluLeuGlyGly 661

1993 GCGCGTTTTCAGGCGCCCAAGCCGAGAGTTGGCGCGA 2031

JUL 26

AA055619 standard; DNA; 2230 BP.

AA055619;

16-OCT-2003 (revised)

25-MAR-2003 (revised)

15-JUL-1994 (first entry)

N meningitidis IM2169 transferrin receptor Tbp2 subunit DNA sequence.

Transferrin receptor; Tbp2 subunit; strain IM2169; meningitis vaccine;

KW iron transport protein; iron chelator; ss.

XX Neisseria meningitidis; (strain IM2169).

OS Neisseria meningitidis; (strain IM2169).

XX Key Location/Qualifiers

FT CDS 60..2195

FT sig_peptide 60..119

FT mat_peptide 120..2192

FT /tag= b

FT /tag= c

FT /product= "Tbp2"

XX FR2692592-A1.

XX 24-DEC-1993.

XX 19-JUN-1992; 92FR-00007493.

XX 19-JUN-1992; 92FR-00007493.

XX (INMR) PASTEUR MERIEUX SERUMS & VACCINS.

XX (TRGE) TRANSGENE SA.

XX Jacobs E, Legrain M, Mazarin V, Bouchon-Rheisen B, Shryvers AB;

XX Bloch M;

XX WPI; 1994-028254/04.

XX P-PSDB; AAR48222.

XX DNA coding for neisseria meningitidis proteins - namely transferrin

XX receptor subunits.

XX Claim 2-7 and 11-12; Page 36-40; 60pp; French.

XX Sequences coding for the Tbp1 and Tbp2 transferrin receptor subunits were

XX isolated from a Neisseria meningitidis strain IM2169 genomic DNA library

XX (see AA055618 and AA055619, respectively). Cells transformed with the DNA

XX can be used for large scale production of the receptor proteins. (Updated

XX on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to

XX standardise OS field)

XX Sequence 2230 BP; 727 A; 483 C; 547 G; 473 T; 0 U; 0 Other;

US-10-735-098-2 (1-725) x AA055619 (1-2230)

OY 649 GlyGlyPheTyrGlyProLysAlaGluGluLeuGlyGly 661

Db 2037 GCGCGTTTTCAGGCGCCCTAAGCCGAGAGTTGGCGCGA 2075

RESULT 27

AA055619 standard; DNA; 2230 BP.

AA055619;

16-OCT-2003 (revised)

30-AUG-1996 (first entry)

Neisseria meningitidis strain IM2169 transferrin receptor Tbp2 gene.

Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;

passive immunisation; immunotherapy; ss.

Neisseria meningitidis; (strain IM2169).

Jacobs

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